SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) NAME: Novo Nordisk A/S
 - (B) STREET: Novo Alle
 - (C) CITY: Bagsvaerd
 - (E) COUNTRY: Dermark
 - (F) POSTAL/CODE (ZIP): 2880
 - (G) TELEPHONE: +45 4444 8888
 - (H) TELEFAX: +45 4449 3256
 - (I) TELEX: \$7304
- (ii) TITLE OF INVENTION: Human Spasmolytic Polypeptide in Glycosylated Form
- (iii) NUMBER OF SEQUENCES: 14
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk

 - (B) COMPUTER: THM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGIH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS; single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
- Glu Lys Pro Ser Pro Cys Gli Cys Ser Arg Leu Ser Pro His Asn Arg
- Thr Asn Cys Gly Phe Pro Gly\lle Thr Ser Asp Gln Cys Phe Asp Asn

29

Gly Cys Cys Phe Asp Ser Ser Val Thr Gly Val Pro Trp Cys Phe His 40

Pro Leu Pro Lys Gln Glu Ser Asp Gln Cys Val Met Glu Val Ser Asp

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	Arg 65	Arg	Asn	Cys	Gly	Tyr 70	Pro	Gly	Ile	Ser	Pro 75	Glu	Glu	Cys	Ala	Ser 80	
i	Arg	Lys	Cys	Cys	Phe 85	Ser	Asn	Phe	Ile	Phe 90	Glu	Val	Pro	Trp	Cys 95	Phe	
1	Phe	Pro	Asn	Ser 100	Val	Glu	Asp	Cys	His 105	Tyr							
(2) I	VFOF	TAM	ON I	FOR S	SEQ I	ED NO): 2:	:								•	
	(i)	(A) (B) (C)	IEN TYI STI	E CHA NGIH: PE: 1 RANDI POLOC	563 NUCLE EDNES	bas eic a SS: s	se pa acid sing]	airs			•						
(3	ii)	MOLE	CULI	TYI	Æ: I	AVIC	(genc	mic)	٠,								
(i :	ii)	HYPC	THE	TCAI	L: NC)									÷		
(7	vi)			SOL			sapi	ens									
()	ix)	(A)		E/KE ATIO			553										
t)		(A)		E/KE ATIC				.de									
i)	ix)	(A)		E/KE ATIC				.de		٠							
. (>	ci)	SEQU	ENCE	DES	CRIF	MOIT	I: SE	D II	NO:	2:	٠						
GAATTO	CAT	т са	AGAA	TAGI	TCA	AACA	ÄGA	AGAI	TACA	AA C	TATO	TTAA	T CA	TACA	CAAT		60
ATAAAC	ŒAC	C AA	AAGA	ATC	AAG	GCI	GII	י דוכ	TTC	GII	TTG	TCC	TTG	ATC			109

Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile

-45

-30

157

-50

GGA TTC TGC TGG GCC CAA CCA GTC ACT GGC GAT GAA TCA TCT GTT GAG

Gly Phe Cys Trp Ala Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu

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								~	30					
										AAC Asn				205
										GAG Glu 1			·	253
										ACG Thr				301
										GGA Gly				3 49
										ccc Pro				397
										AGA Arg 65				445
-										CGG Arg				493 ·
										TTC Phe				541
GAC Asp				TAAC	FICIA	GA			-					563
(2)	INFO	RMAI	MOL	FOR	SEQ	ID N	io: 3	3:						
	((A (B) IE	ngih Pe:	CHAR I: 15 amin GY:	9 am	uno id	TCS: acid	ls			·		
	(ii)	MOL	ECUL	E TY	PE:	prot	ein							

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

-50

Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly Phe Cys Trp Ala

Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile Pro Glu Glu Ser
-35 -30 -25

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Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val Ala Met Ala Glu
-20 -15 -10

Arg Leu Glu Lys Arg Glu Lys Pro Ser Pro Cys Gln Cys Ser Arg Leu
-5 1 5 10

Ser Pro His Asn Arg Thr Asn Cys Gly Phe Pro Gly Ile Thr Ser Asp 15 20 25

Gln Cys Phe Asp Asn Gly Cys Cys Phe Asp Ser Ser Val Thr Gly Val 30 35 40

Pro Trp Cys Phe His Pro Leu Pro Lys Gln Glu Ser Asp Gln Cys Val 45 50 55

Met Glu Val Ser Asp Arg Arg Asn Cys Gly Tyr Pro Gly Ile Ser Pro 60 65 70 75

Glu Glu Cys Ala Ser Arg Lys Cys Cys Phe Ser Asn Phe Ile Phe Glu 80 85 90

Val Pro Trp Cys Phe Phe Pro Asn Ser Val Glu Asp Cys His Tyr 95 100 105

- (2) INFORMATION FOR SEQ ID NO: 4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGIH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - . (A) ORGANISM: synthetic
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGCTGAGCCC CCATAACAG

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGIH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: synthetic

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(xi) SEQUENCE DESCRIPTION: SEQ I	ID NO: 5:	
TGGAAACACC AGGGGAC		17
(2) INFORMATION FOR SEQ ID NO: 6:		
(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		
(vi) ORIGINAL SOURCE: (A) ORGANISM: synthetic		
(xi) SEQUENCE DESCRIPTION: SEQ I	D NO: 6:	
GAGAAACCCT CCCCCTGCCA GTGCTCCAGG C	•	31
(2) INFORMATION FOR SEQ ID NO: 7:		
(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 34 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: CDNA		
(iii) HYPOTHETICAL: NO		
(vi) ORIGINAL SOURCE: (A) ORGANISM: synthetic		
(xi) SEQUENCE DESCRIPTION: SEQ II	O NO: 7:	
TCAGCCIGGA GCACIGGCAG GGGGAGGGIT TCTC	3	4
(2) INFORMATION FOR SEQ ID NO: 8:		
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(iii) HYPOTHETICAL: NO		

(V1	(A) ORGANISM: synthetic	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
GCTGAGA	GAT TGGAGAAGAG AGAGAAACCC TCCCCCT	3
(2) INF	ORMATION FOR SEQ ID NO: 9:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)) MOLECULE TYPE: CDNA	
(iii)) HYPOIHETICAL: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: synthetic	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
TGCGTCAT	TGG AGGTCTC	1
(2) INFO	DRMATION FOR SEQ ID NO: 10:	
(i)	SEQUENCE CHARACTERISTICS: (A) IENGIH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(iii)	HYPOTHETICAL: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: synthetic	
. (xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
AGCACCAI	TGG CACTTCAAAG	20
(2) INFO	RMATION FOR SEQ ID NO: 11:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(11) MOLECULE TYPE: CLAVA	
(iii) HYPOIHETICAL: NO	
(vi) ORIGINAL SOURCE: (A) ORGANISM: synthetic	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:	
GICCCCIGGI GITTCCACCC CCICCCAAAG CAAGAGICGG ATCAGIGCGI CATGGAGGIC	60
(2) INFORMATION FOR SEQ ID NO: 12:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: synthetic	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:	
TGAGACCICC ATGACGCACI GATCCGACIC TIGCITIGGG AGGGGGIGGA AACACCAGGG	60
(2) INFORMATION FOR SEQ ID NO: 13:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOIHETICAL: NO	
(vi) ORIGINAL SOURCE: (A) ORGANISM: synthetic	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
CATGGIGCIT CITCCCGAAC TCTGIGGAAG ACIGCCATTA CTAAGT	46
(2) INFORMATION FOR SEQ ID NO: 14:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 base pairs	

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: synthetic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CIAGACITAG TAATGGCAGT CITCCACAGA GITCGGGAAG AAGCAC